

SEQUENCE LISTING

<110> Wakamiya, N.

<120> Novel Collectin

<130> 19036/37157

<150> JP HEI 10-237611

<151> 1998-08-24

<160> 32

<210> 1

<211> 2024

<212> DNA

<213> Homo Sapiens

<220>

<221> CDS

<222> (670)..(1695)

<400> 1

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aacctcatca cgaatctgca gcggtctgtg gatgacacaa gccaggctat ccagcgaatc      180
aagaacgact ttcaaaatct gcagcaggtt tttcttcaag ccaagaagga cacggattgg      240
ctgaaggaga aagtgcagag cttgcagacg ctggctgccca acaactctgc gttggccaaa      300
gccacaacg acaccttgga ggatatgaac agccagctca actcattcac aggtcagatg      360
gagaacatca ccactatctc tcaagccaac gagcagaacc tgaaagacct gcaggactta      420
cacaaagatg cagagaatag aacagccatc aagttcaacc aactggagga acgcttccag      480
ctctttgaga cggatattgt gaacatcatt agcaatatca gttacacagc ccaccacctg      540
cggacgctga ccagcaatct aaatgaagtc aggaccactt gcacagatac ctttaccaaa      600
cacacagatg atctgacctc cttgaataat accctggcca acatccgttt ggattctgtt      660
tctctcagg atg caa caa gat ttg atg agg tcg agg tta gac act gaa gta      711
          Met Gln Gln Asp Leu Met Arg Ser Arg Leu Asp Thr Glu Val
          1             5             10
gcc aac tta tca gtg att atg gaa gaa atg aag cta gta gac tcc aag      759
Ala Asn Leu Ser Val Ile Met Glu Glu Met Lys Leu Val Asp Ser Lys
    15             20             25             30
cat ggt cag ctc atc aag aat ttt aca ata cta caa ggt cca ccg ggc      807
His Gly Gln Leu Ile Lys Asn Phe Thr Ile Leu Gln Gly Pro Pro Gly
          35             40             45
ccc agg ggt cca aga ggt gac aga gga tcc cag gga ccc cct ggc cca      855
Pro Arg Gly Pro Arg Gly Asp Arg Gly Ser Gln Gly Pro Pro Gly Pro
          50             55             60
act ggc aac aag gga cag aaa gga gag aag ggg gag cct gga cca cct      903
Thr Gly Asn Lys Gly Gln Lys Gly Glu Lys Gly Glu Pro Gly Pro Pro
          65             70             75
ggc cct gcg ggt gag aga ggc cca att gga cca gct ggt ccc ccc gga      951
Gly Pro Ala Gly Glu Arg Gly Pro Ile Gly Pro Ala Gly Pro Pro Gly
          80             85             90
gag cgt ggc ggc aaa gga tct aaa ggc tcc cag ggc ccc aaa ggc tcc      999
Glu Arg Gly Gly Lys Ser Lys Gly Ser Gln Gly Pro Lys Gly Ser
          95             100             105             110
cgt ggt tcc cct ggg aag ccc ggc cct cag ggc ccc agt ggg gac cca      1047
Arg Gly Ser Pro Gly Lys Pro Gly Pro Gln Gly Pro Ser Gly Asp Pro
          115             120             125
ggc ccc ccg ggc cca cca ggc aaa gag gga ctc ccc ggc cct cag ggc      1095
Gly Pro Pro Gly Pro Pro Gly Lys Glu Gly Leu Pro Gly Pro Gln Gly
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cct cct ggc ttc cag gga ctt cag ggc acc gtt ggg gag cct ggg gtg 1143
Pro Pro Gly Phe Gln Gly Leu Gln Gly Thr Val Gly Glu Pro Gly Val
145 150 155
cct gga cct cgg gga ctg cca ggc ttg cct ggg gta cca ggc atg cca 1191
Pro Gly Pro Arg Gly Leu Pro Gly Leu Pro Gly Val Pro Gly Met Pro
160 165 170
ggc ccc aag ggc ccc ccc ggc cct cct ggc cca tca gga gcg gtg gtg 1239
Gly Pro Lys Gly Pro Gly Pro Gly Pro Gly Pro Ser Gly Ala Val Val
175 180 185 190
ccc ctg gcc ctg cag aat gag cca acc ccg gca ccg gag gac aat ggc 1287
Pro Leu Ala Leu Gln Asn Glu Pro Thr Pro Ala Pro Glu Asp Asn Gly
195 200 205
tgc ccg cct cac tgg aag aac ttc aca gac aaa tgc tac tat ttt tca 1335
Cys Pro Pro His Trp Lys Asn Phe Thr Asp Lys Cys Tyr Tyr Phe Ser
210 215 220
gtt gag aaa gaa att ttt gag gat gca aag ctt ttc tgt gaa gac aag 1383
Val Glu Lys Glu Ile Phe Glu Asp Ala Lys Leu Phe Cys Glu Asp Lys
225 230 235
tct tca cat ctt gtt ttc ata aac act aga gag gaa cag caa tgg ata 1431
Ser Ser His Leu Val Phe Ile Asn Thr Arg Glu Glu Gln Gln Trp Ile
240 245 250
aaa aaa cag atg gta ggg aga gag agc cac tgg atc ggc ctc aca gac 1479
Lys Lys Gln Met Val Gly Arg Glu Ser His Trp Ile Gly Leu Thr Asp
255 260 265 270
tca gag cgt gaa aat gaa tgg aag tgg ctg gat ggg aca tct cca gac 1527
Ser Glu Arg Glu Asn Glu Trp Lys Trp Leu Asp Gly Thr Ser Pro Asp
275 280 285
tac aaa aat tgg aaa gct gga cag ccg gat aac tgg ggt cat ggc cat 1575
Tyr Lys Asn Trp Lys Ala Gly Gln Pro Asp Asn Trp Gly His Gly His
290 295 300
ggg cca gga gaa gac tgt gct ggg ttg att tat gct ggg cag tgg aac 1623
Gly Pro Gly Glu Asp Cys Ala Gly Leu Ile Tyr Ala Gly Gln Trp Asn
305 310 315
gat ttc caa tgt gaa gac gtc aat aac ttc att tgc gaa aaa gac agg 1671
Asp Phe Gln Cys Glu Asp Val Asn Asn Phe Ile Cys Glu Lys Asp Arg
320 325 330
gag aca gta ctg tca tct gca tta taacggactg tgatgggatc acatgagcaa 1725
Glu Thr Val Leu Ser Ser Ala Leu
335 340
atcttcagct ctcaaaggca aaggacactc ctttctaatt gcatcacctt ctcacagat 1785
tgaaaaaaaaaaa aaaagcactg aaaaccaatt actgaaaaaaaa aattgacagc tagtgttttt 1845
taccatccgt cattacccaa agacttggga actaaaatgt tccccagggt gatatgctga 1905
ttttcattgt gcacatggac tgaatcacat agattctcct ccgtcagtaa ccgtgcgatt 1965
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<210> 2

<211> 547

<212> PRT

<213> Homo Sapiens

<220>

<223> Deduced Amino Acid Sequence of Novel Collectin from Nucleotide Sequence

<400>2

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Met Tyr Ser His Asn Val Val Ile Met Asn Leu Asn Asn Leu Asn Leu
1 5 10 15
Thr Gln Val Gln Gln Arg Asn Leu Ile Thr Asn Leu Gln Arg Ser Val
20 25 30
Asp Asp Thr Ser Gln Ala Ile Gln Arg Ile Lys Asn Asp Phe Gln Asn
35 40 45
Leu Gln Gln Val Phe Leu Gln Ala Lys Lys Asp Thr Asp Trp Leu Lys
50 55 60

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[illegible]

<210> 3
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Modified Consensus Sequence of collectins Hybridizable with Novel Collectin

<400>3
 Glu Lys Cys Val Glu Met Tyr Thr Asp Gly Lys Trp Asn Asp Arg Asn
 1 5 10 15
 Cys Leu Gln Ser Arg Leu Ala Ile Cys Glu Phe
 20 25

<210> 4
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Reverse Primer for Screening a Novel Collectin.

<400> 4
 caatctgatg agaaggtgat g 21

<210> 5
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Forward Primer for Screening a Novel Collectin.

<400> 5
 acgaggggct ggatgggaca t 21

<210> 6
 <211> 27
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus sequence of three collectins which were reported heretofore

<400>6
 Glu Asp Cys Val Leu Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro
 1 5 10 15
 Cys Ser Thr Ser His Leu Ala Val Cys Glu Phe
 20 25

<210> 7
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> M13 Universal Primer Sequence for Sequencing

<400> 7
 cgacgttgta aaacgacggc cagt 24

<210> 8
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> M13 Reverse Primer Sequence for Sequencing.

<400> 8
 caggaaaca gctatgac

17

<210> 9
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a lambda gt11 Reverse Primer for Sequencing.

<400> 9
 ttgacaccag accaactgggt aatg

24

<210> 10
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a lambda gt11 Forward Primer for Sequencing.

<400> 10
 ggtggcgacg actcctggag cccg

24

<210> 11
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Primer for Screening a Novel Collectin

<400>11
 cgtgaaaatg aatggaagtg g

21

<210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Primer for Screening a Novel Collectin

<400>12
 ttttatccat tgctgttcct c

21

<210> 13
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Primer for Sequencing a Novel Collectin

<400>13
 ctggcagtcc ccgaggtcca g 21

 <210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Primer for Sequencing a Novel Collectin

 <400>14
 gctggtcccc ccgagagcg t 21

 <210> 15
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a 1RC2 Primer for Cap Site Sequencing

 <400> 15
 caaggtacgc cacagcgtat g 21

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Synthetic TGP1 Primer for Cap Site Sequencing

 <400> 16
 tcttcagttt ccctaattccc 20

 <210> 17
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a 2RC2 Primer for Cap Site Sequencing

 <400> 17
 gtacgccaca gcgtatgatg c 21

 <210> 18
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Synthetic TGP2 Primer for Cap Site Sequencing

 <400> 18
 cattcttgac aaacttcata g 21

 <210> 19
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Primer for Screening a Novel Collectin

 <400> 19
 gaagacaagt cttcaactct tg 22

 <210> 20
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Primer for Screening a Novel Collectin

 <400> 20
 ctctgagtct gtgaggccga tc 22

 <210> 21
 <211> 111
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Probe for Screening a Novel Collectin

 <400> 21
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 aaacagatgg tagggagaga gagccactgg atcggcctca cagactcaga g 111

 <210> 22
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Forward Primer for Screening a Novel Collectin

 <400> 22
 gtgcccttg ccctgcagaa tg 22

 <210> 23
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Reverse Primer for Screening a Novel Collectin

 <400> 23
 gcatatcacc ctggggaaca ttttag 26

 <210> 24
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Sequence of a Sense Primer for Screening Beta Actin

 <400> 24
 caagagatgg ccacggctgc t 21

 <210> 25

<211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of an Antisense Primer for Screening Beta Actin

<400> 25
 tccttctgca tcctgtcggc a 21

<210> 26
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Sense Primer for Amplifying the Novel Collectin.

<400> 26
 aaggaaaaa gcggccgcat gcaacaagat ttgatgagg 39

<210> 27
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Reverse Primer for Amplifying the Novel Collectin

<400> 27
 gctctagatt ataatgcaga tgacagtac 29

<210> 28
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Sense Primer for Amplifying the Nockout Gene

<400> 28
 atgcaacaag atttgatgag g 21

<210> 29
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Sequence of a Sense Primer for Amplifying the Nockout Gene

<400> 29
 cctaccggt agaattgacc 20

<210> 30
 <211> 248
 <212> PRT
 <213> Homo sapiens

<220>
 <223> mannan-binding protein (MBP)

<400> 30

Met Ser Leu Phe Pro Ser Leu Pro Leu Leu Leu Ser Met Val Ala
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Ala Ser Tyr Ser Glu Thr Val Thr Cys Glu Asp Ala Gln Lys Thr Cys
 20 25 30

Pro Ala Val Ile Ala Cys Ser Ser Pro Gly Ile Asn Gly Phe Pro Gly
 35 40 45

Lys Asp Gly Arg Asp Gly Thr Lys Gly Glu Lys Gly Glu Pro Gly Gln
 50 55 60

Gly Leu Arg Gly Leu Gln Gly Pro Pro Gly Lys Leu Gly Pro Pro Gly
 65 70 75 80

Asn Pro Gly Pro Ser Gly Ser Pro Gly Pro Lys Gly Gln Lys Gly Asp
 85 90 95

Pro Gly Lys Ser Pro Asp Gly Asp Ser Ser Leu Ala Ala Ser Glu Arg
 100 105 110

Lys Ala Leu Gln Thr Glu Met Ala Arg Ile Lys Lys Trp Leu Thr Phe
 115 120 125

Ser Leu Gly Lys Gln Val Gly Asn Lys Phe Phe Leu Thr Asn Gly Glu
 130 135 140

Ile Met Thr Phe Glu Lys Val Lys Ala Leu Cys Val Lys Phe Gln Ala
 145 150 155 160

Ser Val Ala Thr Pro Arg Asn Ala Ala Glu Asn Gly Ala Ile Gln Asn
 165 170 175

Leu Ile Lys Glu Glu Ala Phe Leu Gly Ile Thr Asp Glu Lys Thr Glu
 180 185 190

Gly Gln Phe Val Asp Leu Thr Gly Asn Arg Leu Thr Tyr Thr Asn Trp
 195 200 205

Asn Glu Gly Glu Pro Asn Asn Ala Gly Ser Asp Glu Asp Cys Val Leu
 210 215 220

Leu Leu Lys Asn Gly Gln Trp Asn Asp Val Pro Cys Ser Thr Ser His
 225 230 235 240

Leu Ala Val Cys Glu Phe Pro Ile
 245

<210> 31

<211> 248

<212> PRT

<213> Homo sapiens

<220>

<223> surfactant protein A (SP-A)

<400> 31

Met Trp Leu Cys Pro Leu Ala Leu Thr Leu Ile Leu Met Ala Ala Ser
 1 5 10 15

Gly Ala Ala Cys Glu Val Lys Asp Val Cys Val Gly Ser Pro Gly Ile
 20 25 30
 Pro Gly Thr Pro Gly Ser His Gly Leu Pro Gly Arg Asp Gly Arg Asp
 35 40 45
 Gly Val Lys Gly Asp Pro Gly Pro Pro Gly Pro Met Gly Pro Pro Gly
 50 55 60
 Glu Thr Pro Cys Pro Pro Gly Asn Asn Gly Leu Pro Gly Ala Pro Gly
 65 70 75 80
 Val Pro Gly Glu Arg Gly Glu Lys Gly Glu Pro Gly Glu Arg Gly Pro
 85 90 95
 Pro Gly Leu Pro Ala His Leu Asp Glu Glu Leu Gln Ala Thr Leu His
 100 105 110
 Asp Phe Arg His Gln Ile Leu Gln Thr Arg Gly Ala Leu Ser Leu Gln
 115 120 125
 Gly Ser Ile Met Thr Val Gly Glu Lys Val Phe Ser Ser Asn Gly Gln
 130 135 140
 Ser Ile Thr Phe Asp Ala Ile Gln Glu Ala Cys Ala Arg Ala Gly Gly
 145 150 155 160
 Arg Ile Ala Val Pro Arg Asn Pro Glu Glu Asn Glu Ala Ile Ala Ser
 165 170 175
 Phe Val Lys Lys Tyr Asn Thr Tyr Ala Tyr Val Gly Leu Thr Glu Gly
 180 185 190
 Pro Ser Pro Gly Asp Phe Arg Tyr Ser Asp Gly Thr Pro Val Asn Tyr
 195 200 205
 Thr Asn Trp Tyr Arg Gly Glu Pro Ala Gly Arg Gly Lys Glu Gln Cys
 210 215 220
 Val Glu Met Tyr Thr Asp Gly Gln Trp Asn Asp Arg Asn Cys Leu Tyr
 225 230 235 240
 Ser Arg Leu Thr Ile Cys Glu Phe
 245

<210> 32

<211> 375

<212> PRT

<213> Homo sapiens

<220>

<223> surfactant protein D (SP-D)

<400> 32

Met Leu Leu Phe Leu Leu Ser Ala Leu Val Leu Leu Thr Gln Pro Leu
 1 5 10 15
 Gly Tyr Leu Glu Ala Glu Met Lys Thr Tyr Ser His Arg Thr Thr Pro
 20 25 30
 Ser Ala Cys Thr Leu Val Met Cys Ser Ser Val Glu Ser Gly Leu Pro
 35 40 45

Gly Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly
 50 55 60
 Asp Pro Gly Leu Pro Gly Ala Ala Gly Gln Ala Gly Met Pro Gly Gln
 65 70 75 80
 Ala Gly Pro Val Gly Pro Lys Gly Asp Asn Gly Ser Val Gly Glu Pro
 85 90 95
 Gly Pro Lys Gly Asp Thr Gly Pro Ser Gly Pro Pro Gly Pro Pro Gly
 100 105 110
 Val Pro Gly Pro Ala Gly Arg Glu Gly Pro Leu Gly Lys Gln Gly Asn
 115 120 125
 Ile Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys
 130 135 140
 Gly Glu Val Gly Ala Pro Gly Met Gln Gly Ser Ala Gly Ala Arg Gly
 145 150 155 160
 Leu Ala Gly Pro Lys Gly Glu Arg Gly Val Pro Gly Glu Arg Gly Val
 165 170 175
 Pro Gly Asn Ala Gly Ala Ala Gly Ser Ala Gly Ala Met Gly Pro Gln
 180 185 190
 Gly Ser Pro Gly Ala Arg Gly Pro Pro Gly Leu Lys Gly Asp Lys Gly
 195 200 205
 Ile Pro Gly Asp Lys Gly Ala Lys Gly Glu Ser Gly Leu Pro Asp Val
 210 215 220
 Ala Ser Leu Arg Gln Gln Val Glu Ala Leu Gln Gly Gln Val Gln His
 225 230 235 240
 Leu Gln Ala Ala Phe Ser Gln Tyr Lys Lys Val Glu Leu Phe Pro Asn
 245 250 255
 Gly Gln Ser Val Gly Glu Lys Ile Phe Lys Thr Ala Gly Phe Val Lys
 260 265 270
 Pro Phe Thr Glu Ala Gln Leu Leu Cys Thr Gln Ala Gly Gly Gln Leu
 275 280 285
 Ala Ser Pro Arg Ser Ala Ala Glu Asn Ala Ala Leu Gln Gln Leu Val
 290 295 300
 Val Ala Lys Asn Glu Ala Ala Phe Leu Ser Met Thr Asp Ser Lys Thr
 305 310 315 320
 Glu Gly Lys Phe Thr Tyr Pro Thr Gly Glu Ser Leu Val Tyr Ser Asn
 325 330 335
 Trp Ala Pro Gly Glu Pro Asn Asp Asp Gly Gly Ser Glu Asp Cys Val
 340 345 350
 Glu Ile Phe Thr Asn Gly Lys Trp Asn Asp Arg Ala Cys Gly Glu Lys
 355 360 365
 Arg Leu Val Val Cys Glu Phe
 370 375